



1

SEQUENCE LISTING

<110> SCHLEHUBER, STEFFEN
<120> MUTEINS OF THE BILIN-BINDING PROTEIN
<130> 029029-0101
<140> 09/980,862
<141> 2002-02-27
<150> PCT/DE00/01873
<151> 2000-06-08
<150> DE 199 26 068.0
<151> 1999-06-08
<160> 29
<170> PatentIn Ver. 2.1
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and fragment of phage coat protein pIII
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<223> mature bilin-binding protein
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<223> amino acids 217-406 of coat protein pIII

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          Met Lys Lys Thr Ala Ile Ala Ile Ala Val
          -20           -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac      99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp
          -10          -5           -1   1           5

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag     147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
          10           15           20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag     195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu
          25           30           35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt     243
Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser
          40           45           50

gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att     291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile
          55           60           65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac     339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr
          70           75           80           85

cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta     387
His Ser Leu Thr Tyr Gly Val Thr Lys Glu Asn Val Phe Asn Val
          90           95           100

ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac     435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr
          105          110          115

gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga     483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg
          120          125          130

agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt     531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu
          135          140          145

atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc     579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe
          150          155          160          165

tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag     627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln
          170          175          180

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ttc gaa aaa tag gct ggc ggc tct ggt ggt tct ggc ggc ggc Phe Glu Lys Gln Ala Gly Gly Ser Gly Gly Ser Gly Gly Gly 185 190 195	675
tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct Ser Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Gly Ser 200 205 210	723
gag gga ggc ggt tcc ggt ggc tct ggt tcc ggt gat ttt gat tat Glu Gly Gly Ser Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr 215 220 225	771
gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp 230 235 240 245	819
gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala 250 255 260	867
act gat tac ggt gct atc gat ggt ttc att ggt gac gtt tcc ggc Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly 265 270 275	915
ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser 280 285 290	963
caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn 295 300 305	1011
ttc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro 310 315 320 325	1059
ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp 330 335 340	1107
aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala 345 350 355	1155
acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys 360 365 370	1203
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<223> a, t, c, g, other or unknown

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<222> (38)
<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

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<223> a, t, c, g, other or unknown

<400> 2
ccatggtaaa tggtgaaaag tcgcataata ccccnknms nnsnnkaagt acggaaagtg 60
          64
cgga

<210> 3
<211> 71
<212> DNA
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<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (46)..(47)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (52)..(53)
<223> a, t, c, g, other or unknown

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ttgacactct t
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<210> 4
<211> 74
<212> DNA
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<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (42)..(43)
<223> a, t, c, g, other or unknown

<220>
<221> modified_base
<222> (54)..(55)
<223> a, t, c, g, other or unknown

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tcaacgtact ctcc                                74

<210> 5
<211> 78
<212> DNA
<213> Artificial Sequence

<220>
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<223> a, t, c, g, other or unknown

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gtatccgatg atgttagtt                                         78

<210> 6
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<220>
<223> Description of Artificial Sequence: Synthetic primer

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<210> 7
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<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 7
caccagtaag gaccatgctt ctggagagca cccagac                                         37

<210> 8
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      oligodeoxynucleotide

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agatcttcc aatcttggag tcaccaactg ggtaggcggt accttc                                         46

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<222> (22)..(783)

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<221> sig_peptide
<222> (22)..(84)

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<222> (85)..(783)
<223> fusion protein of bilin-binding protein, Strep-Tag II
      and albumin-binding domain

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<222> (85)..(606)
<223> mature bilin-binding protein

<220>
<221> misc_feature
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<223> Strep-Tag II affinity tag

<220>
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<222> (637)..(783)
<223> albumin binding domain from Protein G

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      Met Lys Lys Thr Ala Ile Ala Ile Ala Val
      -20                  -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac      99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp
      -10                 -5                  -1     1           5

ggc gtt tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag      147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
      10                  15                  20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag      195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu
      25                  30                  35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt      243
Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser
      40                  45                  50

gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att      291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile
      55                  60                  65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac      339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr
      70                  75                  80                  85

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cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val	
90	95
	100
ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr	
105	110
	115
gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120	125
	130
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135	140
	145
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150	155
	160
	165
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170	175
	180
ttc gaa aaa cca gct agc ctg gct gaa gct aaa gtt ctg gct aac cgt	675
Phe Glu Lys Pro Ala Ser Leu Ala Glu Ala Lys Val Leu Ala Asn Arg	
185	190
	195
gaa ctg gac aaa tac ggt gtt tcc gac tac tac aaa aac ctc atc aac	723
Glu Leu Asp Lys Tyr Gly Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn	
200	205
	210
aac gct aaa acc gtt gaa ggt gtt aaa gct ctg atc gac gaa att ctc	771
Asn Ala Lys Thr Val Glu Gly Val Lys Ala Leu Ile Asp Glu Ile Leu	
215	220
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gca gca ctg ccg taataagctt	793
Ala Ala Leu Pro	
230	

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<210> 10
<211> 17
<212> DNA
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<220>
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      oligodeoxynucleotide

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<210> 11
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
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<400> 11
gactactggg gagccga                                17

<210> 12
<211> 522
<212> DNA
<213> Artificial Sequence

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      nucleic acid sequence

<220>
<221> CDS
<222> (1)..(522)
<223> mutein DigA without fusion parts

<400> 12
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Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
    1          5           10          15

ttc gac tgg tcc cag tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac   96
Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr
    20         25           30

ccc cat cac gag cggt aag tac gga aag tgc gga tgg gct gag tac act  144
Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
    35         40           45

cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc  192
Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
    50          55           60

aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag  240
Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
    65          70           75           80

att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag  288
Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
    85          90           95

ggg gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga  336
Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
    100         105          110

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tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc	384
Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val	
115 120 125	
tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct	432
Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala	
130 135 140	
gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg	480
Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu	
145 150 155 160	
gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat	522
Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn	
165 170	

<210> 13

<211> 76

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic primer

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<220>

<221> modified_base

<222> (38)..(39)

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<220>

<221> modified_base

<222> (47)..(48)

<223> a, t, c, g, t, other or unknown

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<221> modified_base

<222> (50)..(51)

<223> a, t, c, g, t, other or unknown

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<221> modified_base

<222> (53)..(54)

<223> a, t, c, g, t, other or unknown

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<221> modified_base

<222> (56)..(57)

<223> a, t, c, g, t, other or unknown

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gtacggaaaag tgcgga 76

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<210> 14
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<220>
<223> Description of Artificial Sequence: Fragment of
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<221> sig_peptide
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<220>
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<222> (85)..(1209)
<223> fusion protein of bilin-binding protein, Strep-Tag II
      and fragment of phage coat protein pIII, with
      interrupted reading frame

<220>
<221> misc_feature
<222> (85)..(606)
<223> mature bilin-binding protein with interrupted
      reading frame

<220>
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<222> (607)..(636)
<223> Strep-Tag II affinity tag

<220>
<221> misc_feature
<222> (637)..(639)
<223> amber stop codon

<220>
<221> misc_feature
<222> (640)..(1209)
<223> amino acids 217-406 of coat protein pIII

<400> 14
tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg      51
      Met Lys Lys Thr Ala Ile Ala Ile Ala Val
      -20          -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac      99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp
      -10           -5            -1   1           5

```

ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag	147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln	
10 15 20	
tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag	195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu	
25 30 35	
aag tac gga aat taatga tgg gct gag tac act cct gaa ggc aag agt	243
Lys Tyr Gly Asn Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser	
40 45 50	
gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att	291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile	
55 60 65	
gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac	339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr	
70 75 80	
cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta	387
His Ser Leu Thr Tyr Gly Val Thr Lys Glu Asn Val Phe Asn Val	
85 90 95	
ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac	435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr	
100 105 110 115	
gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120 125 130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135 140 145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150 155 160	
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
165 170 175	
ttc gaa aaa tag gct ggc ggc ggc tct ggt ggt tct ggc ggc ggc	675
Phe Glu Lys Gln Ala Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly	
180 185 190 195	
tct gag ggt ggt ggc tct gag ggt ggc ggt tct gag ggt ggc ggc tct	723
Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Ser Glu Gly Gly Ser	
200 205 210	
gag gga ggc ggt tcc ggt ggt ggc tct ggt tcc ggt gat ttt gat tat	771
Glu Gly Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Asp Phe Asp Tyr	
215 220 225	

gaa aag atg gca aac gct aat aag ggg gct atg acc gaa aat gcc gat	819
Glu Lys Met Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp	
230 235 240	
gaa aac gcg cta cag tct gac gct aaa ggc aaa ctt gat tct gtc gct	867
Glu Asn Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala	
245 250 255	
act gat tac ggt gct atc gat ggt ttc att ggt gac gtt tcc ggc	915
Thr Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
260 265 270 275	
ctt gct aat ggt aat ggt gct act ggt gat ttt gct ggc tct aat tcc	963
Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser	
280 285 290	
caa atg gct caa gtc ggt gac ggt gat aat tca cct tta atg aat aat	1011
Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu Met Asn Asn	
295 300 305	
tcc cgt caa tat tta cct tcc ctc cct caa tcg gtt gaa tgt cgc cct	1059
Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val Glu Cys Arg Pro	
310 315 320	
ttt gtc ttt ggc gct ggt aaa cca tat gaa ttt tct att gat tgt gac	1107
Phe Val Phe Gly Ala Gly Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp	
325 330 335	
aaa ata aac tta ttc cgt ggt gtc ttt gcg ttt ctt tta tat gtt gcc	1155
Lys Ile Asn Leu Phe Arg Gly Val Phe Ala Phe Leu Leu Tyr Val Ala	
340 345 350 355	
acc ttt atg tat gta ttt tct acg ttt gct aac ata ctg cgt aat aag	1203
Thr Phe Met Tyr Val Phe Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys	
360 365 370	
gag tct taataagctt	1219
Glu Ser	

<210> 15
<211> 522
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Mutein DigA
nucleic acid sequence

<220>
<221> CDS
<222> (1)..(522)
<223> mutein DigA16 without fusion parts

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Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
1 5 10 15

ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg tac Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr 20 25 30	96
ccc gat cat att acg aag tac gga aag tgc gga tgg gct gag tac act Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr 35 40 45	144
cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac ggc Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly 50 55 60	192
aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc aag Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys 65 70 75 80	240
att gga aag atc tac cac agc tac act att gga ggt gtg acc cag gag Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu 85 90 95	288
ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc gga Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly 100 105 110	336
tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg gtc Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val 115 120 125	384
tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc gct Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala 130 135 140	432
gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa ctg Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu 145 150 155 160	480
gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn 165 170	522

<210> 16
<211> 1380
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fragment of
synthetic pBBP21 nucleic acid sequence

<220>
<221> CDS
<222> (22) .. (636)

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<220>
<221> sig_peptide
<222> (22)..(84)

<220>
<221> mat_peptide
<222> (85)..(636)
<223> fusion protein of bilin-binding protein and Strep-Tag II

<220>
<221> CDS
<222> (658)..(1365)

<220>
<221> sig_peptide
<222> (658)..(717)

<220>
<221> mat_peptide
<222> (718)..(1365)
<223> DsbC protein

<400> 16
tctagataac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg      51
          Met Lys Lys Thr Ala Ile Ala Ile Ala Val
          -20                  -15

gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac      99
Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp
          -10                 -5                  -1     1      5

ggc tgc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag      147
Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
          10                  15                  20

tac cat ggt aaa tgg tgg gaa gtc gcc aaa tac ccc aac tca gtt gag      195
Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr Pro Asn Ser Val Glu
          25                  30                  35

aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt      243
Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser
          40                  45                  50

gtc aaa gtt tcg aac tac cac gta atc cac ggc aag gaa tac ttt att      291
Val Lys Val Ser Asn Tyr His Val Ile His Gly Lys Glu Tyr Phe Ile
          55                  60                  65

gaa gga act gcc tac cca gtt ggt gac tcc aag att gga aag atc tac      339
Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr
          70                  75                  80                  85

cac agc ctg act tac gga ggt gtc acc aag gag aac gta ttc aac gta      387
His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu Asn Val Phe Asn Val
          90                  95                  100

ctc tcc act gac aac aag aac tac atc atc gga tac tac tgc aaa tac      435
Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr
          105                 110                 115

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gac gag gac aag aag gga cac caa gac ttc gtc tgg gtg ctc tcc aga	483
Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val Trp Val Leu Ser Arg	
120	125
130	
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt	531
Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu	
135	140
145	
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc	579
Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe	
150	155
160	165
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag	627
Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln	
170	175
180	
ttc gaa aaa taataagctt cggaaaggatt t atg aag aaa ggt ttt atg ttg	678
Phe Glu Lys	
Met Lys Lys Gly Phe Met Leu	
-20	-15
ttt act ttg tta gcg gcg ttt tca ggc ttt gct cag gct gat gac gcg	726
Phe Thr Leu Leu Ala Ala Phe Ser Gly Phe Ala Gln Ala Asp Asp Ala	
-10	-5
-1	1
gca att caa caa acg tta gcc aaa atg ggc atc aaa agc agc gat att	774
Ala Ile Gln Gln Thr Leu Ala Lys Met Gly Ile Lys Ser Ser Asp Ile	
5	10
15	
cag ccc gcg cct gta gct ggc atg aag aca gtt ctg act aac agc ggc	822
Gln Pro Ala Pro Val Ala Gly Met Lys Thr Val Leu Thr Asn Ser Gly	
20	25
30	35
gtg ttg tac atc acc gat gat ggt aaa cat atc att cag ggg cca atg	870
Val Leu Tyr Ile Thr Asp Asp Gly Lys His Ile Ile Gln Gly Pro Met	
40	45
50	
tat gac gtt agt ggc acg gct ccg gtc aat gtc acc aat aag atg ctg	918
Tyr Asp Val Ser Gly Thr Ala Pro Val Asn Val Thr Asn Lys Met Leu	
55	60
65	
tta aag cag ttg aat gcg ctt gaa aaa gag atg atc gtt tat aaa gcg	966
Leu Lys Gln Leu Asn Ala Leu Glu Lys Glu Met Ile Val Tyr Lys Ala	
70	75
80	
ccg cag gaa aaa cac gtc atc acc gtg ttt act gat att acc tgt ggt	1014
Pro Gln Glu Lys His Val Ile Thr Val Phe Thr Asp Ile Thr Cys Gly	
85	90
95	
tac tgc cac aaa ctg cat gag caa atg gca gac tac aac gcg ctg ggg	1062
Tyr Cys His Lys Leu His Glu Gln Met Ala Asp Tyr Asn Ala Leu Gly	
100	105
110	115
atc acc gtg cgt tat ctt gct ttc ccg cgcc cag ggg ctg gac agc gat	1110
Ile Thr Val Arg Tyr Leu Ala Phe Pro Arg Gln Gly Leu Asp Ser Asp	
120	125
130	

gca gag aaa gaa atg aaa gct atc tgg tgt gcg aaa gat aaa aac aaa	1158
Ala Glu Lys Glu Met Lys Ala Ile Trp Cys Ala Lys Asp Lys Asn Lys	
135 140 145	
gcg ttt gat gat gtg atg gca ggt aaa agc gtc gca cca gcc agt tgc	1206
Ala Phe Asp Asp Val Met Ala Gly Lys Ser Val Ala Pro Ala Ser Cys	
150 155 160	
gac gtg gat att gcc gac cat tac gca ctt ggc gtc cag ctt ggc gtt	1254
Asp Val Asp Ile Ala Asp His Tyr Ala Leu Gly Val Gln Leu Gly Val	
165 170 175	
agc ggt act ccg gca gtt gtg ctg agc aat ggc aca ctt gtt ccg ggt	1302
Ser Gly Thr Pro Ala Val Val Leu Ser Asn Gly Thr Leu Val Pro Gly	
180 185 190 195	
tac cag ccg ccg aaa gag atg aaa gaa ttc ctc gac gaa cac caa aaa	1350
Tyr Gln Pro Pro Lys Glu Met Lys Glu Phe Leu Asp Glu His Gln Lys	
200 205 210	
atg acc agc ggt aaa taattcgcgt agctt	1380
Met Thr Ser Gly Lys	
215	

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<210> 17
<211> 2009
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fragment of
      synthetic pBBP27 nucleic acid sequence

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<222> (23)..(1999)

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<221> sig_peptide
<222> (23)..(85)

<220>
<221> mat_peptide
<222> (86)..(1999)
<223> fusion protein of alkaline phosphatase, linker peptide
      Pro-Pro-Ser-Ala, mutein DigA16 and Strep-Tag II

<220>
<221> misc_feature
<222> (86)..(1435)
<223> mature part of alkaline phosphatase

<220>
<221> misc_feature
<222> (1436)..(1447)
<223> linker peptide Pro-Pro-Ser-Ala

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<220>
<221> misc_feature
<222> (1448)..(1969)
<223> mutein DigA16

<220>
<221> misc_feature
<222> (1970)..(1999)
<223> Strep-Tag II affinity tag

<400> 17
tctagaacat ggagaaaata aa gtg aaa caa agc act att gca ctg gca ctc 52
          Val Lys Gln Ser Thr Ile Ala Leu Ala Leu
          -20                  -15

tta ccg tta ctg ttt acc cct gtg aca aaa gcc cgg aca cca gaa atg 100
Leu Pro Leu Leu Phe Thr Pro Val Thr Lys Ala Arg Thr Pro Glu Met
          -10                 -5           -1   1           5

cct gtt ctg gaa aac cgg gct gct cag ggc gat att act gca ccc ggc 148
Pro Val Leu Glu Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly
          10                  15           20

ggt gct cgc cgt tta acg ggt gat cag act gcc gct ctg cgt gat tct 196
Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser
          25                  30           35

ctt agc gat aaa cct gca aaa aat att att ttg ctg att ggc gat ggg 244
Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly
          40                  45           50

atg ggg gac tcg gaa att act gcc gca cgt aat tat gcc gaa ggt gcg 292
Met Gly Asp Ser Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala
          55                  60           65

ggc ggc ttt ttt aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac 340
Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr
          70                  75           80           85

act cac tat gcg ctg aat aaa acc ggc aaa ccg gac tac gtc acc 388
Thr His Tyr Ala Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr
          90                  95           100

gac tcg gct gca tca gca acc gcc tgg tca acc ggt gtc aaa acc tat 436
Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr
          105                110           115

aac ggc gcg ctg ggc gtc gat att cac gaa aaa gat cac cca acg att 484
Asn Gly Ala Leu Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile
          120                125           130

ctg gaa atg gca aaa gcc gca ggt ctg gcg acc ggt aac gtt tct acc 532
Leu Glu Met Ala Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr
          135                140           145

gca gag ttg cag gat gcc acg ccc gct gcg ctg gtg gca cat gtg acc 580
Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr
          150                155           160           165

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tcg cgc aaa tgc tac ggt ccg agc gcg acc agt gaa aaa tgt ccg ggt	628
Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly	
170	175
180	
aac gct ctg gaa aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt	676
Asn Ala Leu Glu Lys Gly Gly Lys Ser Ile Thr Glu Gln Leu Leu	
185	190
195	
aac gct cgt gcc gac gtt acg ctt ggc ggc ggc gca aaa acc ttt gct	724
Asn Ala Arg Ala Asp Val Thr Leu Gly Gly Ala Lys Thr Phe Ala	
200	205
210	
gaa acg gca acc gct ggt gaa tgg cag gga aaa acg ctg cgt gaa cag	772
Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln	
215	220
225	
gca cag gcg cgt ggt tat cag ttg gtg agc gat gct gcc tca ctg aat	820
Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn	
230	235
240	245
tcg gtg acg gaa gcg aat cag caa aaa ccc ctg ctt ggc ctg ttt gct	868
Ser Val Thr Glu Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala	
250	255
260	
gac ggc aat atg cca gtg cgc tgg cta gga ccg aaa gca acg tac cat	916
Asp Gly Asn Met Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His	
265	270
275	
ggc aat atc gat aag ccc gca gtc acc tgt acg cca aat ccg caa cgt	964
Gly Asn Ile Asp Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg	
280	285
290	
aat gac agt gta cca acc ctg gcg cag atg acc gac aaa gcc att gaa	1012
Asn Asp Ser Val Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu	
295	300
305	
ttg ttg agt aaa aat gag aaa ggc ttt ttc ctg caa gtt gaa ggt gcg	1060
Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala	
310	315
320	325
tca atc gat aaa cag gat cat gct gcg aat cct tgt ggg caa att ggc	1108
Ser Ile Asp Lys Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly	
330	335
340	
gag acg gtc gat ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct	1156
Glu Thr Val Asp Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala	
345	350
355	
aaa aag gag ggt aac acg ctg gtc ata gtc acc gct gat cac gcc cac	1204
Lys Lys Glu Gly Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His	
360	365
370	
gcc agc cag att gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag	1252
Ala Ser Gln Ile Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln	
375	380
385	

gcg cta aat acc aaa gat ggc gca gtg atg gtg atg agt tac ggg aac Ala Leu Asn Thr Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn 390 395 400 405	1300
tcc gaa gag gat tca caa gaa cat acc ggc agt cag ttg cgt att gcg Ser Glu Glu Asp Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala 410 415 420	1348
gcg tat ggc ccg cat gcc gcc aat gtt gtt gga ctg acc gac cag acc Ala Tyr Gly Pro His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr 425 430 435	1396
gat ctc ttc tac acc atg aaa gcc gct ctg ggg ctg aaa ccg cct agc Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu Gly Leu Lys Pro Pro Ser 440 445 450	1444
gct gac gtg tac cac gac ggt gcc tgg ccc gaa gtc aag cca gtc gac Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp 455 460 465	1492
aac ttc gac tgg tcc cag tac cat ggt aaa tgg tgg cag gtc gcc gcg Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala 470 475 480 485	1540
tac ccc gat cat att acg aag tac gga aag tgc gga tgg gct gag tac Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr 490 495 500	1588
act cct gaa ggc aag agt gtc aaa gtt tcg cgc tac tct gta atc cac Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His 505 510 515	1636
ggc aag gaa tac ttt tcc gaa ggt acc gcc tac cca gtt ggt gac tcc Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser 520 525 530	1684
aag att gga aag atc tac cac agc tac act att gga ggt gtg acc cag Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln 535 540 545	1732
gag ggt gta ttc aac gta ctc tcc act gac aac aag aac tac atc atc Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile 550 555 560 565	1780
gga tac ttt tgc tcg tac gac gag gac aag aag gga cac atg gac ttg Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu 570 575 580	1828
gtc tgg gtg ctc tcc aga agc atg gtc ctt act ggt gaa gcc aag acc Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr 585 590 595	1876
gct gtc gag aac tac ctt atc ggc tcc cca gta gtc gac tcc cag aaa Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys 600 605 610	1924

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ctg gta tac agt gac ttc tct gaa gcc gcc tgc aag gtc aac aat agc      1972
Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn Ser
  615                      620                      625

aac tgg tct cac ccg cag ttc gaa aaa taataagctt                         2009
Asn Trp Ser His Pro Gln Phe Glu Lys
  630                      635

<210> 18
<211> 2005
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fragment of
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<222> (22)..(1998)

<220>
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<222> (22)..(84)

<220>
<221> mat_peptide
<222> (85)..(1998)
<223> fusion protein of mutein DigA16, Strep-Tag II, linker
      peptide Gly(5) and alkaline phosphatase

<220>
<221> misc_feature
<222> (85)..(606)
<223> mutein DigA16

<220>
<221> misc_feature
<222> (607)..(636)
<223> Strep-Tag II affinity tag

<220>
<221> misc_feature
<222> (637)..(651)
<223> linker peptide Gly-Gly-Gly-Gly-Gly

<220>
<221> misc_feature
<222> (652)..(1998)
<223> alkaline phosphatase without signalling sequence and
      N-terminal Arg

<400> 18
tctagataaac gagggcaaaa a atg aaa aag aca gct atc gcg att gca gtg      51
      Met Lys Lys Thr Ala Ile Ala Ile Ala Val
      -20                  -15

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gca ctg gct ggt ttc gct acc gta gcg cag gcc gac gtg tac cac gac Ala Leu Ala Gly Phe Ala Thr Val Ala Gln Ala Asp Val Tyr His Asp -10 -5 -1 1 5	99
ggt gcc tgt ccc gaa gtc aag cca gtc gac aac ttc gac tgg tcc cag Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln 10 15 20	147
tac cat ggt aaa tgg tgg cag gtc gcc gcg tac ccc gat cat att acg Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr Pro Asp His Ile Thr 25 30 35	195
aag tac gga aag tgc gga tgg gct gag tac act cct gaa ggc aag agt Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser 40 45 50	243
gtc aaa gtt tcg cgc tac tct gta atc cac ggc aag gaa tac ttt tcc Val Lys Val Ser Arg Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser 55 60 65	291
gaa ggt acc gcc tac cca gtt ggt gac tcc aag att gga aag atc tac Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr 70 75 80 85	339
cac agc tac act att gga ggt gtg acc cag gag ggt gta ttc aac gta His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val 90 95 100	387
ctc tcc act gac aac aag aac tac atc atc gga tac ttt tgc tcg tac Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr 105 110 115	435
gac gag gac aag aag gga cac atg gac ttg gtc tgg gtg ctc tcc aga Asp Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg 120 125 130	483
agc atg gtc ctt act ggt gaa gcc aag acc gct gtc gag aac tac ctt Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu 135 140 145	531
atc ggc tcc cca gta gtc gac tcc cag aaa ctg gta tac agt gac ttc Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe 150 155 160 165	579
tct gaa gcc gcc tgc aag gtc aac aat agc aac tgg tct cac ccg cag Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln 170 175 180	627
ttc gaa aaa ggt ggc ggc ggt ggt aca cca gaa atg cct gtt ctg gaa Phe Glu Lys Gly Gly Gly Gly Thr Pro Glu Met Pro Val Leu Glu 185 190 195	675
aac cgg gct gct cag ggc gat att act gca ccc ggc ggt gct cgc cgt Asn Arg Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg 200 205 210	723

tta acg ggt gat cag act gcc gct ctg cgt gat tct ctt agc gat aaa	771
Leu Thr Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys	
215 220 225	
cct gca aaa aat att att ttg ctg att ggc gat ggg atg ggg gac tcg	819
Pro Ala Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser	
230 235 240 245	
gaa att act gcc gca cgt aat tat gcc gaa ggt gcg ggc ggc ttt ttt	867
Glu Ile Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe	
250 255 260	
aaa ggt ata gat gcc tta ccg ctt acc ggg caa tac act cac tat gcg	915
Lys Gly Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala	
265 270 275	
ctg aat aaa acc ggc aaa ccg gac tac gtc acc gac tcg gct gca	963
Leu Asn Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala	
280 285 290	
tca gca acc gcc tgg tca acc ggt gtc aaa acc tat aac ggc gcg ctg	1011
Ser Ala Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu	
295 300 305	
ggc gtc gat att cac gaa aaa gat cac cca acg att ctg gaa atg gca	1059
Gly Val Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala	
310 315 320 325	
aaa gcc gca ggt ctg gcg acc ggt aac gtt tct acc gca gag ttg cag	1107
Lys Ala Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln	
330 335 340	
gat gcc acg ccc gct gcg ctg gtg gca cat gtg acc tcg cgc aaa tgc	1155
Asp Ala Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys	
345 350 355	
tac ggt ccg agc gcg acc agt gaa aaa tgt ccg ggt aac gct ctg gaa	1203
Tyr Gly Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu	
360 365 370	
aaa ggc gga aaa gga tcg att acc gaa cag ctg ctt aac gct cgt gcc	1251
Lys Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala	
375 380 385	
gac gtt acg ctt ggc ggc gca aaa acc ttt gct gaa acg gca acc	1299
Asp Val Thr Leu Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr	
390 395 400 405	
gct ggt gaa tgg cag gga aaa acg ctg cgt gaa cag gca cag gcg cgt	1347
Ala Gly Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg	
410 415 420	
ggc tat cag ttg gtg agc gat gct gcc tca ctg aat tcg gtg acg gaa	1395
Gly Tyr Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu	
425 430 435	

gcg aat cag caa aaa ccc ctg ctt ggc ctg ttt gct gac ggc aat atg Ala Asn Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met 440 445 450	1443
cca gtg cgc tgg cta gga ccg aaa gca acg tac cat ggc aat atc gat Pro Val Arg Trp Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp 455 460 465	1491
aag ccc gca gtc acc tgt acg cca aat ccg caa cgt aat gac agt gta Lys Pro Ala Val Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val 470 475 480 485	1539
cca acc ctg gcg cag atg acc gac aaa gcc att gaa ttg ttg agt aaa Pro Thr Leu Ala Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys 490 495 500	1587
aat gag aaa ggc ttt ttc ctg caa gtt gaa ggt gcg tca atc gat aaa Asn Glu Lys Gly Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys 505 510 515	1635
cag gat cat gct gcg aat cct tgt ggg caa att ggc gag acg gtc gat Gln Asp His Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp 520 525 530	1683
ctc gat gaa gcc gta caa cgg gcg ctg gaa ttc gct aaa aag gag ggt Leu Asp Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly 535 540 545	1731
aac acg ctg gtc ata gtc acc gct gat cac gcc cac gcc agc cag att Asn Thr Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile 550 555 560 565	1779
gtt gcg ccg gat acc aaa gct ccg ggc ctc acc cag gcg cta aat acc Val Ala Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr 570 575 580	1827
aaa gat ggc gca gtg atg gtg atg agt tac ggg aac tcc gaa gag gat Lys Asp Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp 585 590 595	1875
tca caa gaa cat acc ggc agt cag ttg cgt att gcg gcg tat ggc ccg Ser Gln Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro 600 605 610	1923
cat gcc gcc aat gtt gtt gga ctg acc gac cag acc gat ctc ttc tac His Ala Ala Asn Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr 615 620 625	1971
acc atg aaa gcc gct ctg ggg ctg aaa taagctt Thr Met Lys Ala Ala Leu Gly Leu Lys 630 635	2005

<210> 19
<211> 396
<212> PRT
<213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic pBBP20
 amino acid sequence

<400>	19			
Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala				
-20	-15	-10		
Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val				
-5	-1	1	5	10
Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp				
15	20	25		
Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly				
30	35	40		
Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr				
45	50	55		
His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro				
60	65	70	75	
Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly				
80	85	90		
Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys				
95	100	105		
Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly				
110	115	120		
His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly				
125	130	135		
Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val				
140	145	150	155	
Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys				
160	165	170		
Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Lys Ala Gly				
175	180	185		
Gly Gly Ser Gly Gly Ser Gly Gly Ser Glu Gly Gly Ser Gly				
190	195	200		
Glu Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly				
205	210	215		
Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala				
220	225	230	235	
Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser				
240	245	250		
Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala				
255	260	265		

Ile Asp Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly
 270 275 280

Ala Thr Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly
 285 290 295

Asp Gly Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro
 300 305 310 315

Ser Leu Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly
 320 325 330

Lys Pro Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg
 335 340 345

Gly Val Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe
 350 355 360

Ser Thr Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 365 370 375

<210> 20

<211> 254

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
 synthetic pBBP22 amino acid sequence

<400> 20

Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 -20 -15 -10Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
 -5 -1 1 5 10Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
 15 20 25Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly
 30 35 40Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr
 45 50 55His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro
 60 65 70 75Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly
 80 85 90Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
 95 100 105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly
 110 115 120

 His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
 125 130 135

 Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
 140 145 150 155

 Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
 160 165 170

 Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Pro Ala Ser
 175 180 185

 Leu Ala Glu Ala Lys Val Leu Ala Asn Arg Glu Leu Asp Lys Tyr Gly
 190 195 200

 Val Ser Asp Tyr Tyr Lys Asn Leu Ile Asn Asn Ala Lys Thr Val Glu
 205 210 215

 Gly Val Lys Ala Leu Ile Asp Glu Ile Leu Ala Ala Leu Pro
 220 225 230

 <210> 21
 <211> 174
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic DigA
 amino acid sequence

 <400> 21
 Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
 1 5 10 15

 Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr
 20 25 30

 Pro His His Glu Arg Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
 35 40 45

 Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
 50 55 60

 Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
 65 70 75 80

 Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
 85 90 95

 Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
 100 105 110

 Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
 115 120 125

Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
 130 135 140

Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
 145 150 155 160

Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
 165 170

.<210> 22
 <211> 394
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fragment of
 synthetic pBBP24 amino acid sequence

<400> 22
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 -20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
 -5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
 15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Asn Trp Ala
 30 35 40

Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val
 45 50 55

Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly
 60 65 70 75

Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly Val
 80 85 90

Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr
 95 100 105

Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly His Gln
 110 115 120

Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala
 125 130 135

Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser
 140 145 150 155

Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn
 160 165 170

Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Lys Ala Gly Gly Gly
 175 180 185
 Ser Gly Gly Ser Gly Gly Ser Glu Gly Gly Gly Ser Glu Gly
 190 195 200
 Gly Gly Ser Glu Gly Gly Ser Glu Gly Gly Ser Gly Gly Gly
 205 210 215
 Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met Ala Asn Ala Asn Lys
 220 225 230 235
 Gly Ala Met Thr Glu Asn Ala Asp Glu Asn Ala Leu Gln Ser Asp Ala
 240 245 250
 Lys Gly Lys Leu Asp Ser Val Ala Thr Asp Tyr Gly Ala Ala Ile Asp
 255 260 265
 Gly Phe Ile Gly Asp Val Ser Gly Leu Ala Asn Gly Asn Gly Ala Thr
 270 275 280
 Gly Asp Phe Ala Gly Ser Asn Ser Gln Met Ala Gln Val Gly Asp Gly
 285 290 295
 Asp Asn Ser Pro Leu Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu
 300 305 310 315
 Pro Gln Ser Val Glu Cys Arg Pro Phe Val Phe Gly Ala Gly Lys Pro
 320 325 330
 Tyr Glu Phe Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val
 335 340 345
 Phe Ala Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr
 350 355 360
 Phe Ala Asn Ile Leu Arg Asn Lys Glu Ser
 365 370

<210> 23

<211> 174

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mutein DigA16
amino acid sequence

<400> 23

Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
1 5 10 15Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr
20 25 30Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
35 40 45

Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr Ser Val Ile His Gly
 50 55 60

 Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
 65 70 75 80

 Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu
 85 90 95

 Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
 100 105 110

 Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly His Met Asp Leu Val
 115 120 125

 Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
 130 135 140

 Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
 145 150 155 160

 Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
 165 170

<210> 24
 <211> 205
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fragment of
 synthetic pBBP21 amino acid sequence

<400> 24
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 -20 -15 -10

Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
 -5 -1 1 5 10

Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
 15 20 25

Glu Val Ala Lys Tyr Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly
 30 35 40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr
 45 50 55

His Val Ile His Gly Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro
 60 65 70 75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly
 80 85 90

Gly Val Thr Lys Glu Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys
 95 100 105

Asn Tyr Ile Ile Gly Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly
 110 115 120

His Gln Asp Phe Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
 125 130 135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
 140 145 150 155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
 160 165 170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys
 175 180

<210> 25

<211> 236

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
synthetic pBBP21 amino acid sequence

<400> 25

Met Lys Lys Gly Phe Met Leu Phe Thr Leu Leu Ala Ala Phe Ser Gly
 -20 -15 -10 -5Phe Ala Gln Ala Asp Asp Ala Ala Ile Gln Gln Thr Leu Ala Lys Met
 -1 1 5 10Gly Ile Lys Ser Ser Asp Ile Gln Pro Ala Pro Val Ala Gly Met Lys
 15 20 25Thr Val Leu Thr Asn Ser Gly Val Leu Tyr Ile Thr Asp Asp Gly Lys
 30 35 40His Ile Ile Gln Gly Pro Met Tyr Asp Val Ser Gly Thr Ala Pro Val
 45 50 55 60Asn Val Thr Asn Lys Met Leu Leu Lys Gln Leu Asn Ala Leu Glu Lys
 65 70 75Glu Met Ile Val Tyr Lys Ala Pro Gln Glu Lys His Val Ile Thr Val
 80 85 90Phe Thr Asp Ile Thr Cys Gly Tyr Cys His Lys Leu His Glu Gln Met
 95 100 105Ala Asp Tyr Asn Ala Leu Gly Ile Thr Val Arg Tyr Leu Ala Phe Pro
 110 115 120Arg Gln Gly Leu Asp Ser Asp Ala Glu Lys Glu Met Lys Ala Ile Trp
 125 130 135 140

Cys Ala Lys Asp Lys Asn Lys Ala Phe Asp Asp Val Met Ala Gly Lys
 145 150 155

Ser Val Ala Pro Ala Ser Cys Asp Val Asp Ile Ala Asp His Tyr Ala
 160 165 170

Leu Gly Val Gln Leu Gly Val Ser Gly Thr Pro Ala Val Val Leu Ser
 175 180 185

Asn Gly Thr Leu Val Pro Gly Tyr Gln Pro Pro Lys Glu Met Lys Glu
 190 195 200

Phe Leu Asp Glu His Gln Lys Met Thr Ser Gly Lys
 205 210 215

<210> 26

<211> 659

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fragment of
 synthetic pBBP27 amino acid sequence

<400> 26

Val Lys Gln Ser Thr Ile Ala Leu Ala Leu Pro Leu Leu Phe Thr
 -20 -15 -10

Pro Val Thr Lys Ala Arg Thr Pro Glu Met Pro Val Leu Glu Asn Arg
 -5 -1 1 5 10

Ala Ala Gln Gly Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr
 15 20 25

Gly Asp Gln Thr Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala
 30 35 40

Lys Asn Ile Ile Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile
 45 50 55

Thr Ala Ala Arg Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly
 60 65 70 75

Ile Asp Ala Leu Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn
 80 85 90

Lys Lys Thr Gly Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala
 95 100 105

Thr Ala Trp Ser Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val
 110 115 120

Asp Ile His Glu Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala
 125 130 135

Ala Gly Leu Ala Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala
 140 145 150 155
 Thr Pro Ala Ala Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly
 160 165 170
 Pro Ser Ala Thr Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly
 175 180 185
 Gly Lys Gly Ser Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val
 190 195 200
 Thr Leu Gly Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly
 205 210 215
 Glu Trp Gln Gly Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr
 220 225 230 235
 Gln Leu Val Ser Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn
 240 245 250
 Gln Gln Lys Pro Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val
 255 260 265
 Arg Trp Leu Gly Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro
 270 275 280
 Ala Val Thr Cys Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr
 285 290 295
 Leu Ala Gln Met Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu
 300 305 310 315
 Lys Gly Phe Phe Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp
 320 325 330
 His Ala Ala Asn Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp
 335 340 345
 Glu Ala Val Gln Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr
 350 355 360
 Leu Val Ile Val Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala
 365 370 375
 Pro Asp Thr Lys Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp
 380 385 390 395
 Gly Ala Val Met Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln
 400 405 410
 Glu His Thr Gly Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala
 415 420 425
 Ala Asn Val Val Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met
 430 435 440

Lys Ala Ala Leu Gly Leu Lys Pro Pro Ser Ala Asp Val Tyr His Asp
 445 450 455
 Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn Phe Asp Trp Ser Gln
 460 465 470 475
 Tyr His Gly Lys Trp Trp Gln Val Ala Ala Tyr Pro Asp His Ile Thr
 480 485 490
 Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser
 495 500 505
 Val Lys Val Ser Arg Tyr Ser Val Ile His Gly Lys Glu Tyr Phe Ser
 510 515 520
 Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr
 525 530 535
 His Ser Tyr Thr Ile Gly Gly Val Thr Gln Glu Gly Val Phe Asn Val
 540 545 550 555
 Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr
 560 565 570
 Asp Glu Asp Lys Lys Gly His Met Asp Leu Val Trp Val Leu Ser Arg
 575 580 585
 Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu
 590 595 600
 Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe
 605 610 615
 Ser Glu Ala Ala Cys Lys Val Asn Asn Ser Asn Trp Ser His Pro Gln
 620 625 630 635
 Phe Glu Lys

<210> 27
 <211> 659
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fragment of
 synthetic pBBP29 amino acid sequence

<400> 27
 Met Lys Lys Thr Ala Ile Ala Ile Ala Val Ala Leu Ala Gly Phe Ala
 -20 -15 -10
 Thr Val Ala Gln Ala Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val
 -5 -1 1 5 10
 Lys Pro Val Asp Asn Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp
 15 20 25

Gln Val Ala Ala Tyr Pro Asp His Ile Thr Lys Tyr Gly Lys Cys Gly
 30 35 40

Trp Ala Glu Tyr Thr Pro Glu Gly Lys Ser Val Lys Val Ser Arg Tyr
 45 50 55

Ser Val Ile His Gly Lys Glu Tyr Phe Ser Glu Gly Thr Ala Tyr Pro
 60 65 70 75

Val Gly Asp Ser Lys Ile Gly Lys Ile Tyr His Ser Tyr Thr Ile Gly
 80 85 90

Gly Val Thr Gln Glu Gly Val Phe Asn Val Leu Ser Thr Asp Asn Lys
 95 100 105

Asn Tyr Ile Ile Gly Tyr Phe Cys Ser Tyr Asp Glu Asp Lys Lys Gly
 110 115 120

His Met Asp Leu Val Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly
 125 130 135

Glu Ala Lys Thr Ala Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val
 140 145 150 155

Asp Ser Gln Lys Leu Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys
 160 165 170

Val Asn Asn Ser Asn Trp Ser His Pro Gln Phe Glu Lys Gly Gly Gly
 175 180 185

Gly Gly Thr Pro Glu Met Pro Val Leu Glu Asn Arg Ala Ala Gln Gly
 190 195 200

Asp Ile Thr Ala Pro Gly Gly Ala Arg Arg Leu Thr Gly Asp Gln Thr
 205 210 215

Ala Ala Leu Arg Asp Ser Leu Ser Asp Lys Pro Ala Lys Asn Ile Ile
 220 225 230 235

Leu Leu Ile Gly Asp Gly Met Gly Asp Ser Glu Ile Thr Ala Ala Arg
 240 245 250

Asn Tyr Ala Glu Gly Ala Gly Gly Phe Phe Lys Gly Ile Asp Ala Leu
 255 260 265

Pro Leu Thr Gly Gln Tyr Thr His Tyr Ala Leu Asn Lys Lys Thr Gly
 270 275 280

Lys Pro Asp Tyr Val Thr Asp Ser Ala Ala Ser Ala Thr Ala Trp Ser
 285 290 295

Thr Gly Val Lys Thr Tyr Asn Gly Ala Leu Gly Val Asp Ile His Glu
 300 305 310 315

Lys Asp His Pro Thr Ile Leu Glu Met Ala Lys Ala Ala Gly Leu Ala
 320 325 330

Thr Gly Asn Val Ser Thr Ala Glu Leu Gln Asp Ala Thr Pro Ala Ala
 335 340 345
 Leu Val Ala His Val Thr Ser Arg Lys Cys Tyr Gly Pro Ser Ala Thr
 350 355 360
 Ser Glu Lys Cys Pro Gly Asn Ala Leu Glu Lys Gly Gly Lys Gly Ser
 365 370 375
 Ile Thr Glu Gln Leu Leu Asn Ala Arg Ala Asp Val Thr Leu Gly Gly
 380 385 390 395
 Gly Ala Lys Thr Phe Ala Glu Thr Ala Thr Ala Gly Glu Trp Gln Gly
 400 405 410
 Lys Thr Leu Arg Glu Gln Ala Gln Ala Arg Gly Tyr Gln Leu Val Ser
 415 420 425
 Asp Ala Ala Ser Leu Asn Ser Val Thr Glu Ala Asn Gln Gln Lys Pro
 430 435 440
 Leu Leu Gly Leu Phe Ala Asp Gly Asn Met Pro Val Arg Trp Leu Gly
 445 450 455
 Pro Lys Ala Thr Tyr His Gly Asn Ile Asp Lys Pro Ala Val Thr Cys
 460 465 470 475
 Thr Pro Asn Pro Gln Arg Asn Asp Ser Val Pro Thr Leu Ala Gln Met
 480 485 490
 Thr Asp Lys Ala Ile Glu Leu Leu Ser Lys Asn Glu Lys Gly Phe Phe
 495 500 505
 Leu Gln Val Glu Gly Ala Ser Ile Asp Lys Gln Asp His Ala Ala Asn
 510 515 520
 Pro Cys Gly Gln Ile Gly Glu Thr Val Asp Leu Asp Glu Ala Val Gln
 525 530 535
 Arg Ala Leu Glu Phe Ala Lys Lys Glu Gly Asn Thr Leu Val Ile Val
 540 545 550 555
 Thr Ala Asp His Ala His Ala Ser Gln Ile Val Ala Pro Asp Thr Lys
 560 565 570
 Ala Pro Gly Leu Thr Gln Ala Leu Asn Thr Lys Asp Gly Ala Val Met
 575 580 585
 Val Met Ser Tyr Gly Asn Ser Glu Glu Asp Ser Gln Glu His Thr Gly
 590 595 600
 Ser Gln Leu Arg Ile Ala Ala Tyr Gly Pro His Ala Ala Asn Val Val
 605 610 615
 Gly Leu Thr Asp Gln Thr Asp Leu Phe Tyr Thr Met Lys Ala Ala Leu
 620 625 630 635
 Gly Leu Lys

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<210> 28
<211> 174
<212> PRT
<213> Pieris brassicae

<400> 28
Asp Val Tyr His Asp Gly Ala Cys Pro Glu Val Lys Pro Val Asp Asn
 1           5          10          15

Phe Asp Trp Ser Gln Tyr His Gly Lys Trp Trp Glu Val Ala Lys Tyr
 20          25          30

Pro Asn Ser Val Glu Lys Tyr Gly Lys Cys Gly Trp Ala Glu Tyr Thr
 35          40          45

Pro Glu Gly Lys Ser Val Lys Val Ser Asn Tyr His Val Ile His Gly
 50          55          60

Lys Glu Tyr Phe Ile Glu Gly Thr Ala Tyr Pro Val Gly Asp Ser Lys
 65          70          75          80

Ile Gly Lys Ile Tyr His Ser Leu Thr Tyr Gly Gly Val Thr Lys Glu
 85          90          95

Asn Val Phe Asn Val Leu Ser Thr Asp Asn Lys Asn Tyr Ile Ile Gly
100         105         110

Tyr Tyr Cys Lys Tyr Asp Glu Asp Lys Lys Gly His Gln Asp Phe Val
115         120         125

Trp Val Leu Ser Arg Ser Met Val Leu Thr Gly Glu Ala Lys Thr Ala
130         135         140

Val Glu Asn Tyr Leu Ile Gly Ser Pro Val Val Asp Ser Gln Lys Leu
145         150         155         160

Val Tyr Ser Asp Phe Ser Glu Ala Ala Cys Lys Val Asn Asn
165         170

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<210> 29
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      peptide linker

<400> 29
Pro Pro Ser Ala
 1

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